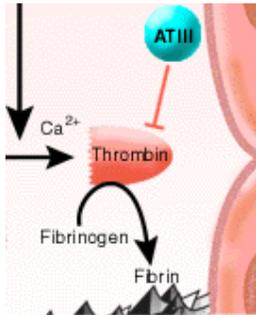


26 April 2000

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A cascade of clotting factors culminates in the formation of a blood clot.

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Mutations and blood clots

Clotting is essential, yet can be fatal. Pathological activation of the clotting cascade can lead to the formation of a blood clot, typically a deep vein thrombosis (DVT) in the legs. This blood clot may then be carried in the bloodstream to the lungs. This is known as a pulmonary embolism and is a medical emergency, being one of the leading causes of sudden death.

After trauma, the formation of a thrombus is essential to stem bleeding. A cascade of pro-enzymes, enzymes and cofactors interact with damaged vessel endothelium to converge on a common pathway with the formation of a fibrin clot. The clot acts a mechanical plug to prevent bleeding and is vital for normal vascular function. Disturbance of this pathway can be deadly - too little clotting results in bleeding disorders such as hemophilia, whereas excessive clotting produces blood clots that can block the lungs.

There are many factors that lead to an excessive propensity to clot, or thrombophilia. These can be classified by: (1) changes in blood vessel wall (2) changes in blood flow and (3) changes in blood constituents. Among the genetic components that underlie problems with blood constituents are mutations of clotting factor genes. These cause a deficiency of the body's natural anticoagulants, such as protein C, protein S, or antithrombin III (see figure). However, the most common inherited mutation that predisposes to thrombosis is the factor V Leiden mutation.

Factor V acts towards the end of the clotting cascade, where it is a co-factor for the Xa-dependant proteolytic cleavage of prothrombin to thrombin. Thrombin then catalyzes the conversion of soluble fibrinogen to a solid fibrin clot. Activated factor V (Va) is kept in check by a serine protease called activated protein C (APC). APC stops factor V from working by cleaving sites on its heavy chain - in particular at the sites Arg506 and Arg306. Thus APC is important in limiting clot formation.

Factor V Leiden is a single point mutation resulting in an amino acid substitution of arginine for glutamine at Arg506. The mutation affects factor V's APC-binding site, therefore preventing factor V inactivation. It is carriers of this APC-resistant factor V that suffer from a propensity to inappropriate clot formation.

What if you are a carrier of factor V Leiden? It is a common mutation, with a prevalence of 2% in Caucasian populations. It is especially found in patients with DVTs and increases the risk of thrombosis during pregnancy or while taking oral contraceptives. It is also associated with an increased risk of miscarriage. Although it is the most important genetic risk factor that we know of, the overall probability of thrombosis is still low with a single mutation. However, with the co-inheritance of other clotting factor polymorphisms

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such as that of prothrombin which increases levels of prothrombin in the blood, the risk of thrombosis now becomes more significant.

Further investigation of the clotting factor mutations will help explain the hereditary basis of thrombophilia. Most importantly however, the main causes of DVT are not inherited but are acquired. Despite our genetic make-up, a healthy lifestyle is our most important weapon for keeping thrombosis at bay.

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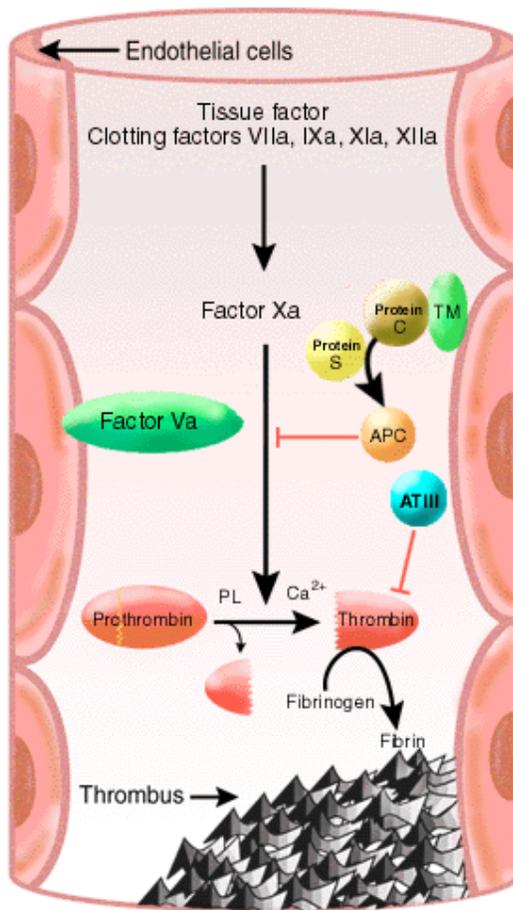
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Mutations and blood clots



Key

Black arrows = activation;
 Red arrows = inactivation;
 APC = activated protein C
 TM = thrombomodulin, a protein bound to endothelial cell membranes to which protein C binds;
 PL = phospholipid;
 Ca²⁺ = calcium;

Each reaction in the coagulation cascade involves the conversion of a clotting factor precursor into an active protease by proteolysis, regulated by cofactors and calcium. The end point is the generation of enough thrombin to catalyze the formation of fibrin, which then polymerizes and crosslinks to form a clot. Under pathological conditions, the mutation in **factor V** renders it resistant to inactivation by APC. Hence mutated factor V pushes the cascade towards excessive blood clot formation. Mutations in the upstream region of the **prothrombin** gene result in increased levels of prothrombin in the blood, again encouraging the formation of a thrombus. Protein C, protein S and antithrombin III all have

anti-coagulant action. Deficiencies of proteins C and S usually result in a syndrome of recurrent venous thrombosis and pulmonary embolism. Deficiency of antithrombin III is usually mild.

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This is a paper which studies the incidence of thrombosis in women during pregnancy and for a 6 week period after giving birth. It found that of the women who suffered from a deep vein thrombosis during this period, a significant proportion had underlying genetic abnormalities. It indicates the risk of thromboembolism for prothrombin mutations is at least as high for that of factor V Leiden. A risk of thrombosis as high as 69% was estimated if both these mutations were co-inherited.

1 : *N Engl J Med* 2000 Feb 10;342(6):374-80

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Prothrombin and factor V mutations in women with a history of thrombosis during pregnancy and the puerperium.

Gerhardt A, Scharf RE, Beckmann MW, Struve S, Bender HG, Pillny M, Sandmann W, Zotz RB

Department of Hemostasis and Transfusion Medicine, Heinrich Heine University Medical Center, Dusseldorf, Germany.

BACKGROUND: Venous thromboembolism is a leading cause of morbidity and mortality during pregnancy and the puerperium. However, the role of mutations in the prothrombin and factor V genes and other thrombophilic abnormalities as risk factors for thromboembolism in women during pregnancy and the puerperium is not known. **METHODS:** In a study of 119 women with a history of venous thromboembolism during pregnancy and the puerperium and 233 age-matched normal women, we measured the activity of antithrombin, protein C, protein S, and lupus anticoagulant. We also performed genetic analyses to detect the G1691A mutation in the factor V gene (factor V Leiden), the G20210A mutation in the prothrombin gene, and the C677T mutation in the methylenetetrahydrofolate reductase gene. Blood samples were obtained at least three months post partum or after the cessation of lactation. **RESULTS:** Among the women with a history of venous thromboembolism, the prevalence of factor V Leiden was 43.7 percent, as compared with 7.7 percent among the normal women (relative risk of venous thromboembolism, 9.3; 95 percent confidence interval, 5.1 to 16.9); that of the G20210A prothrombin-gene mutation, 16.9 percent as compared with 1.3 percent (relative risk, 15.2; 95 percent confidence interval, 4.2 to 52.6); and that of both factor V Leiden and the G20210A prothrombin-gene mutation 9.3 percent as compared with 0 (estimated odds ratio, 107). Assuming an overall risk of 1 in 1500 pregnancies, the risk of thrombosis among carriers of factor V Leiden was 0.2 percent, among carriers of the G20210A prothrombin-gene mutation, 0.5 percent, and among carriers of both defects, 4.6 percent, as calculated in a multivariate analysis. **CONCLUSIONS:** The G20210A prothrombin-gene mutation and factor V Leiden individually are associated with an increased risk of venous thromboembolism during pregnancy and the puerperium, and the risk among women with both mutations is disproportionately higher than that among women with only one mutation.

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Revised: January 10, 2000.

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UniGene is a collection of Genbank sequences that have been organized into clusters - the aim is for each cluster to represent one gene. Expressed Sequence Tags (ESTs) make up most of the clusters. These are short nucleotide sequences (100-400 nt) and so represent only fragments of genes. ESTs are selected and sequenced at random from cDNA libraries derived from a cell line or tissue of interest e.g. a cell line from a family with hereditary thrombophilia. Such rapid production of ESTs enables a much faster rate of progress of gene discovery.

Coagulation factor V has been entered in the text box, click on "go".

UniGene Resources

The UniGene System

UniGene is an experimental system for automatically partitioning GenBank sequences into a non-redundant set of gene-oriented clusters. Each UniGene cluster contains sequences that represent a unique gene, as well as related information such as the tissue types in which the gene has been expressed and map location.

In addition to sequences of well-characterized genes, hundreds of thousands novel expressed sequence tag (EST) sequences have been included. Consequently, the collection may be of use to the community as a resource for gene discovery. UniGene has also been used by experimentalists to select reagents for gene mapping projects and large-scale expression analysis.

However, it should be noted that the procedures for automated sequence clustering are still under development and the results may change from time to time as improvements are made. Feedback from users has been especially useful in identifying problems and we encourage you to report any problems you encounter.

It should also be noted that no attempt has been made to produce contigs or consensus sequences. There are several reasons why the sequences of a set may not actually form a single contig. For example, all of the splicing variants for a gene are put into the same set. Moreover, EST-containing sets often contain 5' and 3' reads from the same cDNA clone, but these sequences do not always overlap.

At present, only sequences from human, rat, and mouse have been processed. These species were chosen because they have the greatest amounts of EST data available. Additional organisms may be added in the future.

A representation of the UniGene datasets is available by [ftp](#).

A description of the UniGene [build procedure](#) is available.

UniGene References

An article about the [UniGene Collection](#) in the [August 1997 NCBI News](#) contains an overview of the project. Although the number of UniGene clusters has changed since that article was written due to improvements in the clustering algorithm, the article provides background information as well as a description of how the collection was used in the Transcript Map project (see Schuler et al., 1996, below).

Additional references include:

Schuler (1997). Pieces of the puzzle: expressed sequence tags and the catalog of human genes. *J Mol Med* 75(10),694-698. [[PubMed](#)]

Schuler et al. (1996). A gene map of the human genome. *Science* 274, 540-546. [[PubMed](#)] [[SCIENCE On-line](#)]

Boguski & Schuler (1995). ESTablishing a human transcript map. *Nature Genetics* 10, 369-371. [[PubMed](#)] [[Full Text](#)]

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Click on the UniGene reference number for coagulation factor V.

2 records satisfy the query **coagulation factor v** for the organism **Homo sapiens**

UniGene	Description	Symbol
Hs.21016	coagulation factor C (Limulus polyphemus) homology (cochlin)	COCH
Hs.30054	coagulation factor V (proaccelerin, labile factor)	F5

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 Search for

Hs.30054 *Homo sapiens* **F5**

Gene hunters use UniGene for discovering new family members of their gene of interest in the same species, and for finding functionally equivalent genes in other species. We are interested in the factor V protein. There is a similar protein in the fruit fly called neurexin IV. This protein has a stretch of 124 amino acids that have a 31% identity to human factor V protein. Click on the protein identifier (PID) to find out about the function of neurexin.

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Coagulation factor V (proaccelerin, labile factor)
SEE ALSO

LocusLink: 2153
OMIM: 227400

SELECTED MODEL ORGANISM PROTEIN SIMILARITIES

<i>H. sapiens</i> :	PID:g488110 - coagulation factor V	100 % / 2223 aa
<i>M. musculus</i> :	PID:g3219691 - Murine coagulation factor V	70 % / 2219 aa
<i>R. norvegicus</i> :	PIR:A35210 - ferroxidase	36 % / 623 aa
<i>D. melanogaster</i> :	PID:g1518221 - neurexin IV	31 % / 124 aa
<i>C. elegans</i> :	PID:g1086659 - repetitive region	30 % / 247 aa
<i>S. cerevisiae</i> :	PID:e239834 - ORF YNR044w	25 % / 276 aa

MAPPING INFORMATION

Chromosome: 1
Cytogenetic Position: 1q23
Gene Map 98: Marker stGDB:194742 , Interval D1S196-D1S210
Gene Map 98: Marker M14335 , Interval D1S196-D1S210
Gene Map 98: Marker W88564 , Interval D1S196-D1S210
Gene Map 98: Marker SGC32933 , Interval D1S196-D1S210
Gene Map 98: Marker stSG17607 , Interval D1S196-D1S210
Whitehead map: EST376226, Chr.1
dbSTS entries: G25791

EXPRESSION INFORMATION

cdNA sources: Liver and Spleen, gall bladder, heart, kidney, lung, placenta, prostate
SAGE : [Gene to Tag mapping](#)

mRNA/GENE SEQUENCES (5)

L32779	Human coagulation factor V gene	P A S
M16967	Human coagulation factor V mRNA, complete cds	P A S
M14335	Human coagulation factor V mRNA, complete cds	P A S
Z99572	Human DNA sequence from PAC 86F14 on chromosome 1q23-1q24. Contains coagulation factor V, ESTs and STS	P S
NM_000130	Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5) mRNA	

EST SEQUENCES (10 of 50)[\[Show all ESTs\]](#)

AI207246	cDNA clone IMAGE:1758878		3' read	1.3 kb	P C
AI274530	cDNA clone IMAGE:1981178	Kidney	3' read	1.2 kb	P A C
R84234	cDNA clone IMAGE:194571		5' read	1.2 kb	P
R71060	cDNA clone IMAGE:142726	Placenta	3' read	1.2 kb	S
H74282	cDNA clone IMAGE:229509		5' read	1.1 kb	P S
H74283	cDNA clone IMAGE:229509		3' read	1.1 kb	P S
AA976662	cDNA clone IMAGE:1585363	Lung	3' read	1.1 kb	P A S C
H75674	cDNA clone IMAGE:211332		5' read	1.0 kb	P
H69028	cDNA clone IMAGE:211332		3' read	1.0 kb	P A S
H78713	cDNA clone IMAGE:229431		5' read	1.0 kb	P

Key to Symbols

- P** Has similarity to known **P**roteins (after translation)
- A** Contains a poly-**A**denylation signal
- S** Contains a mapped **S**equence-tagged site (STS)
- C** Clone source is a **C**GAP library

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Whereas factor V is a clotting factor, neurexin is a protein involved in the blood brain barrier in the fly. To find out more about neurexin and to find whether there is any correlation of function with that of factor V, click on the medline reference number.

1: [CAA60383](#). (X86685) neurexin ...[gi:1518221] [PubMed](#), [Related Sequences](#), [Nucleotide](#), [LinkOut](#)

```

LOCUS       CAA60383     1283 aa             INV             14-JAN-1997
DEFINITION   neurexin IV [Drosophila melanogaster].
ACCESSION   CAA60383
PID         gl1518221
VERSION     CAA60383.1  GI:1518221
DBSOURCE    embl locus DMNRXGENE, accession X86685.1
KEYWORDS    .
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
             Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
             Drosophilidae; Drosophila.
REFERENCE   1 (residues 1 to 1283)
AUTHORS     Baumgartner,S., Littleton,J.T., Broadie,K., Bhat,M.A., Harbecke,R.,
             Lengyel,J.A., Chiquet-Ehrismann,R., Prokop,A. and Bellen,H.J.
TITLE       A Drosophila neurexin is required for septate junction and
             blood-nerve barrier formation and function
JOURNAL     Cell 87 (6), 1059-1068 (1996)
MEDLINE     97133213
REFERENCE   2 (residues 1 to 1283)
AUTHORS     Baumgartner,S.W.
TITLE       Direct Submission
JOURNAL     Submitted (26-APR-1995) S.W. Baumgartner, FMI, PO Box 2543, 4002
             Basel, SWITZERLAND
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             /db_xref="taxon:7227"
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             /clone_lib="pNB40"
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             sig_peptide     1..28
             CDS             1..1283

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             /db_xref="FLYBASE:FBgn0013997"
             /db_xref="SPTREMBL:Q94887"
             /coded_by="X86685.1:279..4130"
  
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```

ORIGIN
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121 ysdggefwrw yvnpstsepqm fkgnsdgsni hynvfevpii aqwvripnr whdrismrve
181 lygodyisen lyfngtglvr ydlrrepits tkesirfrfk tafangvmmmy srgtqgdyya
241 lqlkdknmvl nldlgsrvmt slsvgslldd nvwhdvvisr nqrdiifsvd rvivrgriqg
301 eftrlnlnre lyggvgnvqg eglivqmfms gcleniyfns tnfirvmkds telgegylft
361 rvntiyacps ppiypvtftt rssfvrkgy ensqrlnvsf yfrtyeetgv mlhhdffysgg
421 ylkvflefgk vkidlkvdkd arilidnydd qfndgkwhsf visieknrli lnidqrpmtt
481 tksmqvata qyyiaggkdk ngfvgcmrli svdgnyklpq dwvkgeevcc gddvvvdacq
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781 tlgplrcegd dlfsnvvtfr iadasinlpp fdmghsgdiy leftrtqens vifhatgptd
841 yiklslnngn klqfyqgags gplgvnvgts yhlndnnwht vsvernrkea rlvvdgsika
901 evreppgpvr alhltsdlvi gattdyrdgy vgcirallln gkmvdlkeys krglygistg
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1201 lvdeeklrka ynevsvlla clvilflil ilmffligry lhrhkgdylt hedqgadgad
1261 dpddavlhst tghqvrkte ifi

//

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Neurexin IV is a protein needed for the proper formation of junctions and barriers between cells. Perhaps the amino acid sequence similarity that is observed in the fly neurexin protein and human factor V represents a common domain that is important in cell binding.

1: *Cell* 1996 Dec 13;87(6):1059-68

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A *Drosophila* neurexin is required for septate junction and blood-nerve barrier formation and function.

Baumgartner S, Littleton JT, Broadie K, Bhat MA, Harbecke R, Lengyel JA, Chiquet-Ehrismann R, Prokop A, Bellen HJ

Friedrich Miescher-Institute, Basel, Switzerland.

Septate and tight junctions are thought to seal neighboring cells together and to function as barriers between epithelial cells. We have characterized a novel member of the neurexin family, Neurexin IV (NRX), which is localized to septate junctions (SJs) of epithelial and glial cells. NRX is a transmembrane protein with a cytoplasmic domain homologous to glycoporphin C, a protein required for anchoring protein 4.1 in the red blood cell. Absence of NRX results in mislocalization of Coracle, a *Drosophila* protein 4.1 homolog, at SJs and causes dorsal closure defects similar to those observed in coracle mutants. nrx mutant embryos are paralyzed, and electrophysiological studies indicate that the lack of NRX in glial-glia SJs causes a breakdown of the blood-brain barrier. Electron microscopy demonstrates that nrx mutants lack the ladder-like intercellular septa characteristic of pleated SJs (pSJs). These studies identify NRX as the first transmembrane protein of SJ and demonstrate a requirement for NRX in the formation of septate-junction septa and intercellular barriers.

MeSH Terms:

- Amino Acid Sequence
- Animal
- Blood Cells
- Blotting, Northern
- Blotting, Western
- Cloning, Molecular
- Drosophila*/embryology*
- DNA Mutational Analysis
- Electrophysiology
- Epithelium/physiology
- Genetic Markers
- Membrane Proteins/genetics*
- Microscopy, Electron
- Molecular Sequence Data
- Nerve Tissue Proteins/genetics*
- Nervous System/physiology
- Nervous System/embryology
- Nervous System/chemistry
- Nervous System Physiology
- Neuroglia/physiology
- Neurons/physiology
- Sequence Analysis, DNA
- Support, Non-U.S. Gov't
- Support, U.S. Gov't, P.H.S.
- Tight Junctions/ultrastructure
- Tight Junctions/physiology
- Tight Junctions/chemistry*

Substances:

- Nerve Tissue Proteins
- Membrane Proteins
- Genetic Markers
- neurexin IV

Secondary source id:

- GENBANK/U18017
- GENBANK/Z42448
- GENBANK/U17905
- GENBANK/U18000
- GENBANK/T27170

o GENBANK/X86685

Grant support:

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PMID: 8978610, UI: 97133213

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